

Sub B1

[illegible]

- DOCKET  
ON INFO  
(201)  
201) 9

(2) INFORMATION FOR SEQ ID NO:1:

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 82..771

- 111

TTT ACG GTC AGT TTG GCA TTA CAG ATC ATC AAT TTG GGA AAC AGC TAT 159  
Phe Thr Val Ser Leu Ala Leu Gln Ile Ile Asn Leu Gly Asn Ser Tyr 25

15

AAA AGA GAG AAA CAT AAC GGC GGT AGA GAG GAA GTC ACC AAG GTT GCC 207  
Gln Arg Glu Lys His Asn Gly Gly Arg Glu Glu Val Thr Lys Val Ala 40

30

ACT CAG AAG CAC CGA CAG TCA CCG CTC AAC TGG ACC TCC AGT CAT TTC 255  
Thr Gln Lys His Arg Gln Ser Pro Leu Asn Trp Thr Ser Ser His Phe 55

45

GGA GAG GTG ACT GGG AGC GCC GAG GGC TGG GGG CCG GAG GAG CCG CTC 303  
Gly Glu Val Thr Gly Ser Ala Glu Gly Trp Gly Pro Glu Glu Pro Leu 70

60

CCC TAC TCC CGG GCT TTC GGA GAG GGT GCG TCC GCG CGG CCG CGC TGC 351  
Pro Tyr Ser Arg Ala Phe Gly Glu Gly Ala Ser Ala Arg Pro Arg Cys 90

75

TGC AGG AAC GGC GGT ACC TGC GTG CTG GGC AGC TTC TGC GTG TGC CCG 399  
Cys Arg Asn Gly Gly Thr Cys Val Leu Gly Ser Phe Cys Val Cys Pro 105

95

GCC CAC TTC ACC GGC CGC TAC TGC GAG CAT GAC CAG AGG CGC AGT GAA 447  
Ala His Phe Thr Gly Arg Tyr Cys Glu His Asp Gln Arg Arg Ser Glu 120

110

TGC GGC GCC CTG GAG CAC GGA GCC TGG ACC CTC CGC GCC TGC CAC CTC 495  
Cys Gly Ala Leu Glu His Gly Ala Trp Thr Leu Arg Ala Cys His Leu 135

125

TGC AGG TGC ATC TTC GGG GCC CTG CAC TGC CTC CCC CTC CAG ACG CCT 543  
Cys Arg Cys Ile Phe Gly Ala Leu His Cys Leu Pro Leu Gln Thr Pro 150

140

GAC CGC TGT GAC CCG AAA GAC TTC CTG GCC TCC AAC GCT CAC GGG CCG 591  
Asp Arg Cys Asp Pro Lys Asp Phe Leu Ala Ser His Ala His Gly Pro 170

155

AGC GCC GGG GGC GCG CCC AGC CTG CTA CTC TTG CTG CCC TGC GCA ACT 639  
Ser Ala Gly Gly Ala Pro Ser Leu Leu Leu Leu Leu Pro Cys Ala Thr 185

175

CCT GCA CCG GCC TCC TGC GCC CGG ATG CGC CCG CGC ACC CTC GGT CCC 687  
Pro Ala Pro Ala Ser Cys Ala Arg Met Arg Pro Arg Thr Leu Gly Pro 200

190

TGG TCC CTT CCG TCC TCC AGC GGG AGC GGC GCC CCT GCG GAA GGC CCG 735  
Trp Ser Leu Pro Ser Ser Ser Gly Ser Gly Ala Pro Ala Glu Gly Arg 215

205

GAC TTG GGC ATC GCC TTT AAT TTT CTA TGT TGT AAA TAA 774  
Asp Leu Gly Ile Ala Phe Asn Phe Leu Cys Cys Lys 230

220

225

230

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 230 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Trp Arg His His Val Arg Leu Leu Phe Thr Val Ser Leu Ala  
1 5 10 15  
Leu Gln Ile Ile Asn Leu Gly Asn Ser Tyr Gln Arg Glu Lys His Asn  
20 25 30  
Gly Gly Arg Glu Glu Val Thr Lys Val Ala Thr Gln Lys His Arg Gln  
35 40 45  
Ser Pro Leu Asn Trp Thr Ser Ser His Phe Gly Glu Val Thr Gly Ser  
50 55 60  
Ala Glu Gly Trp Gly Pro Glu Glu Pro Leu Pro Tyr Ser Arg Ala Phe  
65 70 75 80  
Gly Glu Gly Ala Ser Ala Arg Pro Arg Cys Cys Arg Asn Gly Gly Thr  
85 90 95  
Cys Val Leu Gly Ser Phe Cys Val Cys Pro Ala His Phe Thr Gly Arg  
100 105 110  
Tyr Cys Glu His Asp Gln Arg Arg Ser Glu Cys Gly Ala Leu Glu His  
115 120 125  
Gly Ala Trp Thr Leu Arg Ala Cys His Leu Cys Arg Cys Ile Phe Gly  
130 135 140  
Ala Leu His Cys Leu Pro Leu Gln Thr Pro Asp Arg Cys Asp Pro Lys  
145 150 155 160  
Asp Phe Leu Ala Ser His Ala His Gly Pro Ser Ala Gly Gly Ala Pro  
165 170 175  
Ser Leu Leu Leu Leu Leu Pro Cys Ala Thr Pro Ala Pro Ala Ser Cys  
180 185 190  
Ala Arg Met Arg Pro Arg Thr Leu Gly Pro Trp Ser Leu Pro Ser Ser  
195 200 205  
Ser Gly Ser Gly Ala Pro Ala Glu Gly Arg Asp Leu Gly Ile Ala Phe  
210 215 220  
Asn Phe Leu Cys Cys Lys  
225 230

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACTCTTGAT CCAATTGGG AAACAGCTATC AAAGA

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "PRIMER"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TACAACTCTA GACTATTATT TACAACATAG AAAATTAAAG GC

42

- (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "PRIMER"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACTCTTGGAT CCGCCATCAT GACCTGGAGG CACCAT

36

- (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "PRIMER"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TACAACCAGC TGCTATTATT TACAACATAG

30

- (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 188 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Asp Cys Arg Lys Met Ala Arg Phe Ser Tyr Ser Val Ile Trp Ile  
 1 5 10 15

